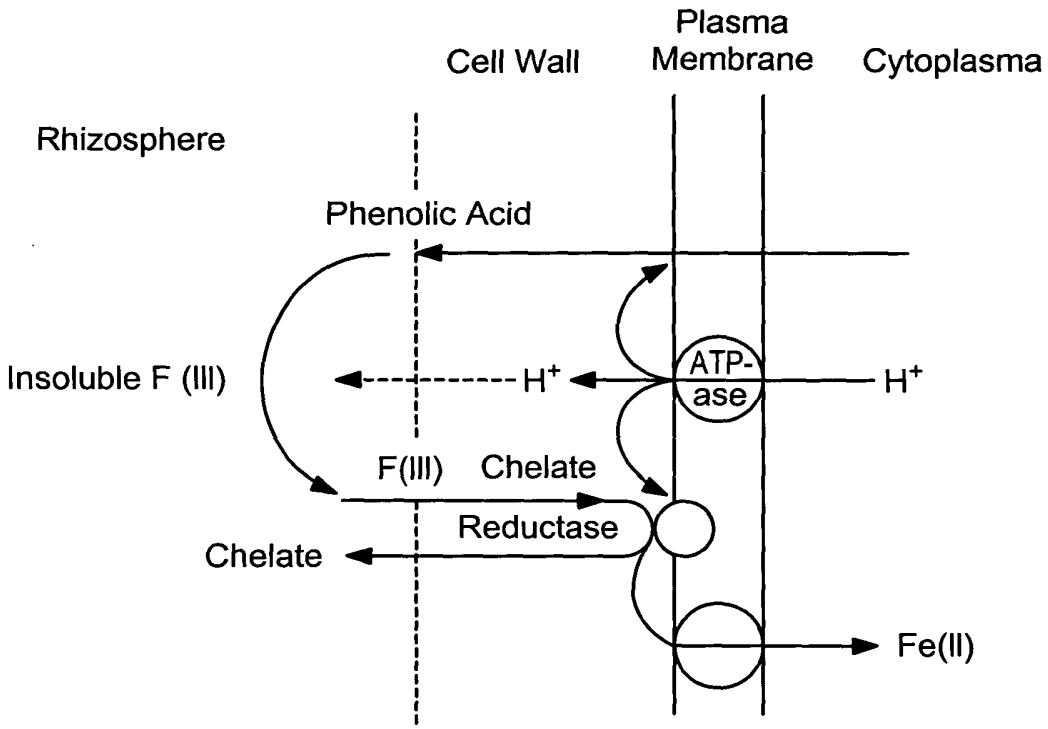
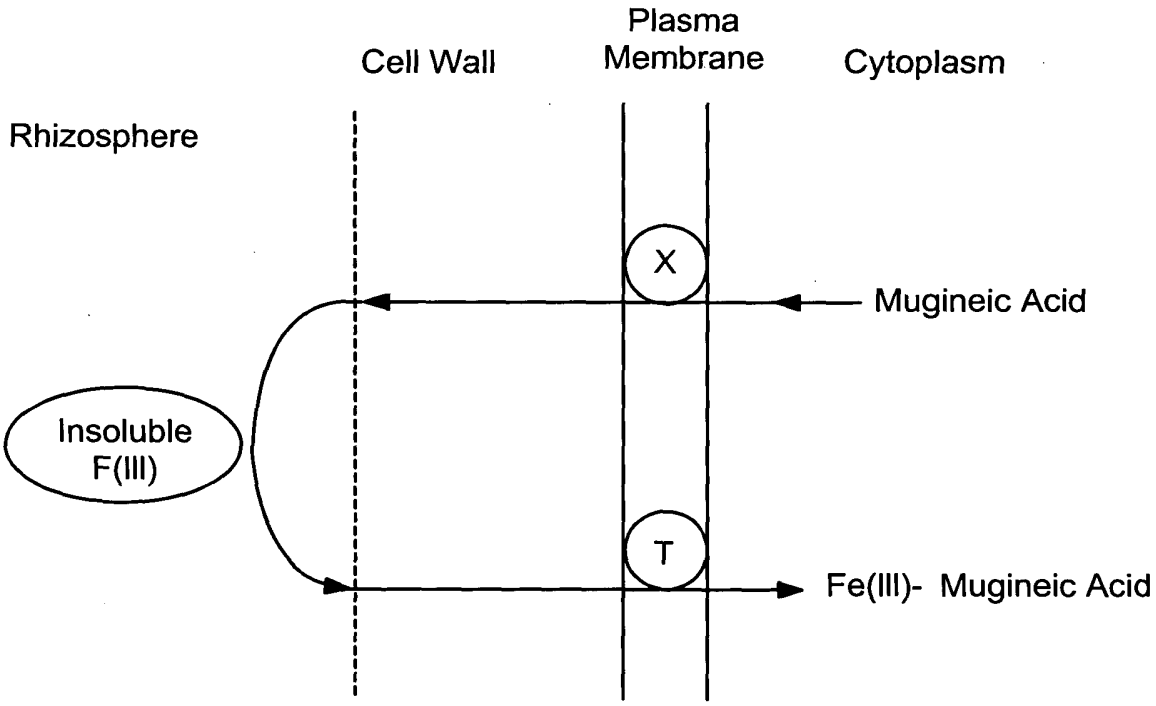


FIG. 1



Two Kinds of Fe-Uptake Mechanisms in Higher Plants

FIG. 2

Seq 37

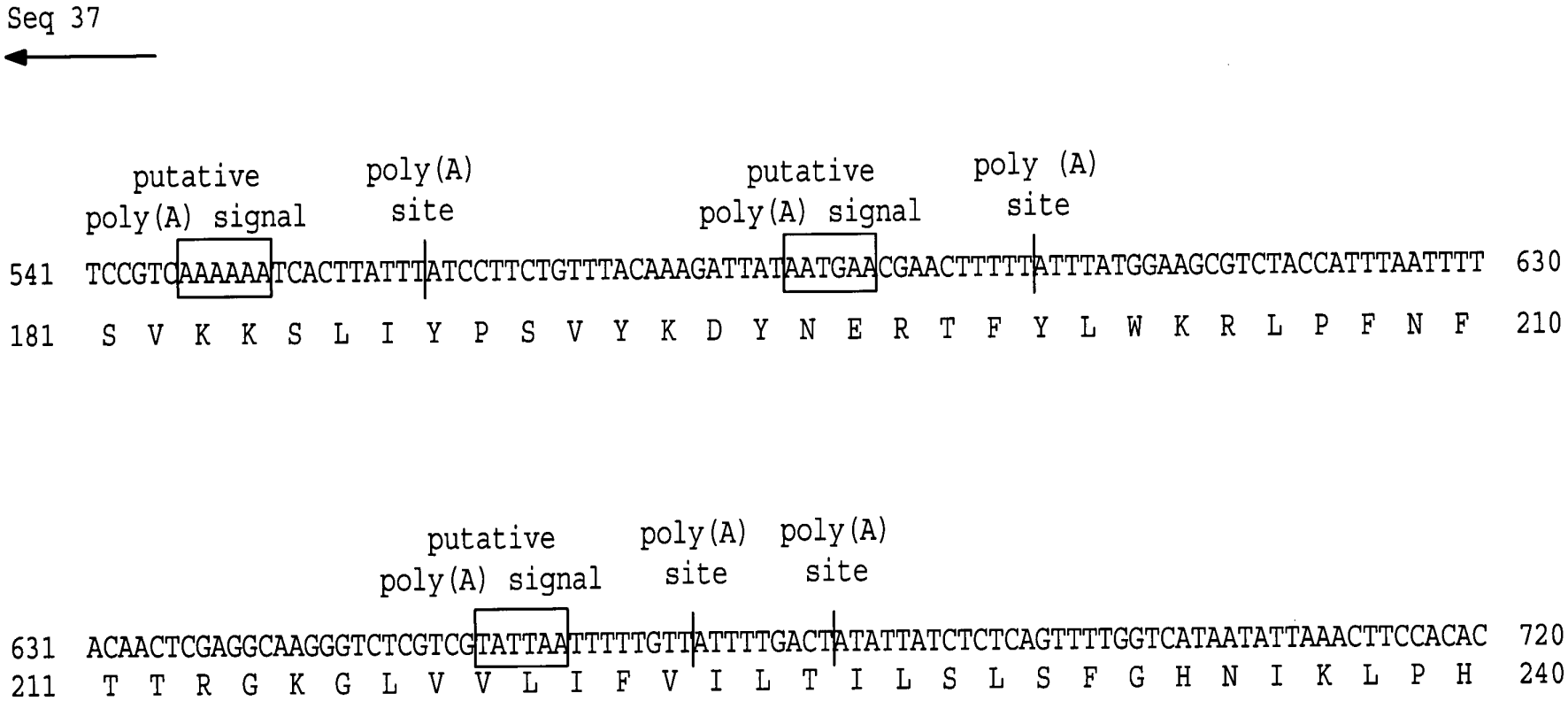

putative poly(A) signal
poly(A) site
putative poly(A) signal
poly (A) site
541 TCCGTCAAAAAATCACTTATTTATCCTTCTGTTTACAAAGATTATAATGAACGAACTTTTTATTTATGGAAGCGTCTACCATTTAATTTT 630
181 S V K K S L I Y P S V Y K D Y N E R T F Y L W K R L P F N F 210
putative poly(A) signal
poly(A) site
poly(A) site
631 ACAACTCGAGGCAAGGGTCTCGTCGTATTAATTTTTGTTATTTTGACTATATTATCTCTCAGTTTTGGTCATAATATTAAACTTCCACAC 720
211 T T R G K G L V V L I F V I L T I L S L S F G H N I K L P H 240

FIG. 3

```
   1 ATGGTTAGAACCCGTGTATTATTCTGGTTATTTATATCTTTTTTTGCTACGGTTCAATCG   60
  61 AGTGCTAGACTTATTAGCACTTCATGTATTTCCCAAGCTGCGCTATACCAATTTGGATGT  120
 121 TCTAGTAAATCTAAAAGTTGCTACTGTAAAAACATCAATTGGCTGGGTTCAGTGACAGCA  180
 181 TGTGCCTATGAGAATTCCAAATCTAACAAAACACTAGACAGCGCCTTAATGAAGTTAGCA  240
 241 TCCCAATGTTCAAGCATCAAAGTTTATACTTTAGAGGACATGAAGAATATTTATTTAAAT  300
 301 GCGTCAAATTATTTGAGAGCACCTGAGAAAAGTGATAAAAAAACCGTGGTTAGTCAACCG  360
 361 CTCATGGCGAACGAGACAGCGTATCATTATTATTATGAGGAAAATTATGGTATCCATCTT  420
 421 AACCTAATGCGCTCTCAATGGTGGGGTTGGGGTGTGGTGTTCTTGTGGGTGGGTGTGGTT  480
 481 ACTGCAGCCACTATCTTGAACATTCTGAAAAGGGTGTTTGGTAAGAACATCATGGCAAAC  540
 541 TCCGTCAAAAAATCACTTATTTATCCTTCTGTTTACAAAGATTATAATGAACGAACTTTT  600
 601 TATTTATGGAAGCGTCTACCATTTAATTTTACAACTCGAGGCAAGGGTCTCGTCGTATTA  660
 661 ATTTTTTGTTATTTTGACTATATTATCTCTCAGTTTTGGTCATAATATTAAACTTCCACAC  720
 721 CCATATGATAGGCCCAGATGGAGAAGAAGTATGGCCTTTGTGAGTCGTAGAGCAGACTTG  780
 781 ATGGCCATTGCACTTTTCCCAGTAGTCTATCTATTCGGAATAAGAAATAATCCCTTCATC  840
 841 CCTATAACAGGGCTTTCCTTTTCTACATTTAATTTCTATCATAAATGGTCTGCCTACGTT  900
 901 TGTTTCATGTTGGCCGTTGTACACTCAATTGTCATGACCGCCTCGGGAGTGAAAAGAGGT  960
 961 GTGTTTCAAAGTCTGGTTAGGAAATTTTACTTTAGGTGGGGTATAGTGGCAACGATATTA 1020
1021 ATGTCTATTATTATTTTCCAAAGTGAAAAAGTATTTAGAAATAGAGGGTATGAGATATTC 1080
1081 CTTCTTATTCATAAAGCGATGAATATTATGTTCATTATTGCCATGTACTACCATTGTCAC 1140
1141 ACCCTGGGCTGGATGGGTTGGATTTGGTCAATGGCTGGTATTTTATGCTTTGATAGATTC 1200
1201 TGCAGGATTGTTAGAATAATCATGAATGGTGGCTTGAAAACTGCTACTTTGAGTACCACT 1260
1261 GATGATTCTAATGTTATTAAAATTTCAGTAAAAAAACCAAAGTTTTTCAAGTACCAAGTA 1320
1321 GGAGCTTTCGCATACATGTATTTCTTATCACCAAAAAGTGCATGGTTCTATAGTTTCCAA 1380
1381 TCACATCCATTTACAGTATTATCGGAACGACACCGTGATCCAAACAATCCAGATCAATTG 1440
1441 ACGATGTACGTAAAGGCAAATAAAGGTATCACTCGAGTTTTGTTATCGAAAGTTCTAAGT 1500
1501 GCTCCAAATCATACTGTTGATTGTAAAATATTCCTTGAAGGCCCATATGGTGTAACGGTT 1560
1561 CCACATATCGCTAAGCTAAAAAGAAATCTGGTAGGTGTAGCCGCTGGTTTGGGTGTTGCG 1620
1621 GCTATTTATCCGCACTTTGTCGAATGTTTACGGTTACCATCTACTGATCAACTTCAGCAT 1620
1681 AAATTTTACTGGATTGTTAATGACCTATCCCATTTGAAATGGTTTGAAAATGAATTGCAA 1740
1741 TGGTTAAAGGAGAAAAGTTGTGAAGTCTCAGTCATATATACTGGTTCCAGTGTTGAGGAC 1800
1801 ACAAATTCAGATGAGAGTACAAAAGGTTTTGATGATAAAGAAGAAAGCGAAATCACTGTT 1860
1861 GAATGTCTCAATAAAAGACCTGATTTGAAAGAACTAGTGCGCTCGGAAATAAAACTCTCA 1920
1921 GAACTAGAGAATAATAATATTACCTTTTATTCCTGCGGGCCAGCAACGTTTAACGACGAT 1980
1981 TTTAGAAATGCAGTGGTCCAAGGTATAGACTCTTCCTTGAAGATTGACGTTGAACTAGAA 2040
2041 GAAGAAAGTTTTACATGGT                                           2059
```

FIG. 4

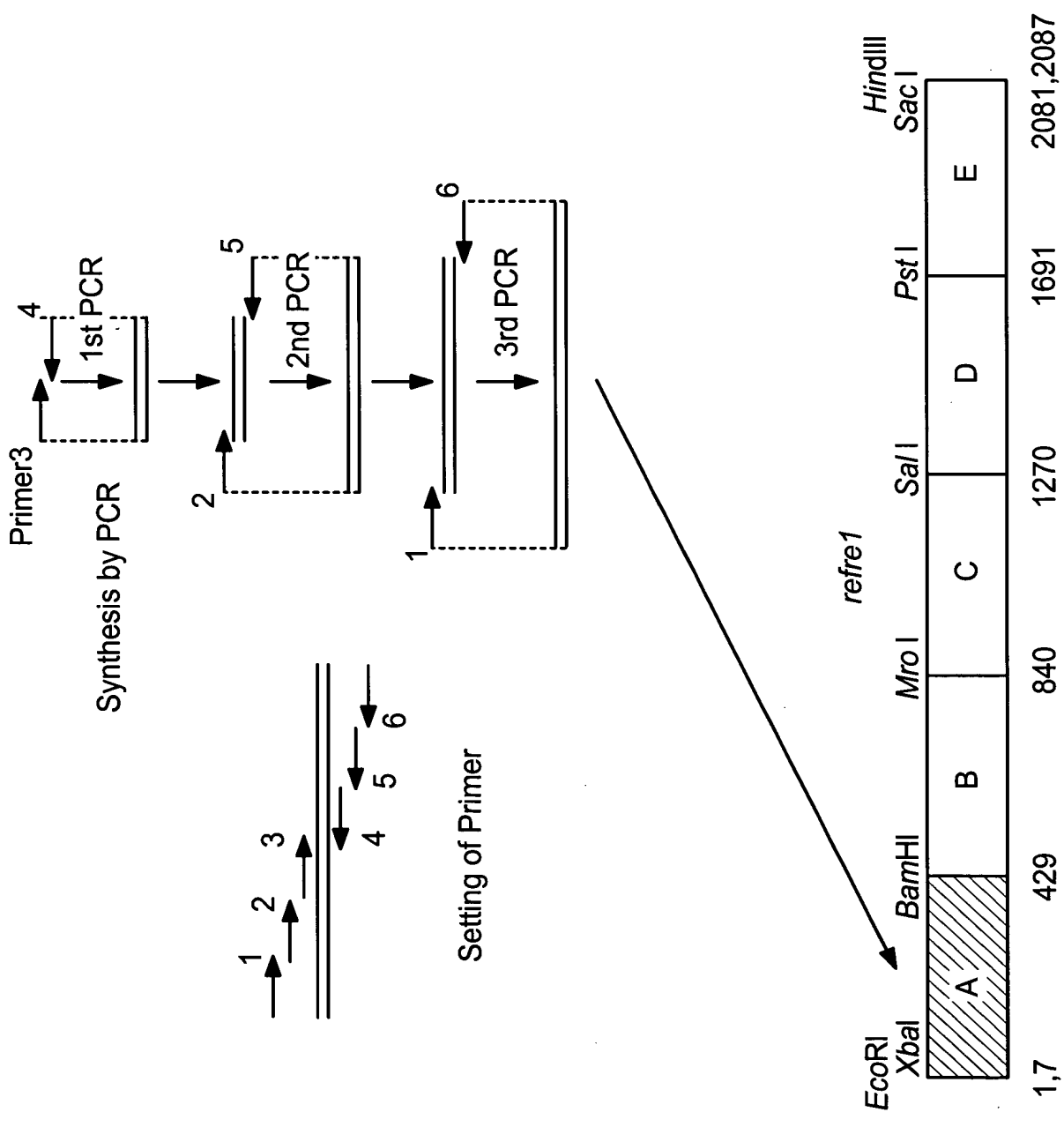

Primer3
Synthesis by PCR
1st PCR
2nd PCR
3rd PCR
Setting of Primer
refre1
EcoRI
XbaI
BamHI
MroI
SalI
PstI
SacI
HindIII
A
B
C
D
E
1,7
429
840
1270
1691
2081,2087

FIG. 5

Sequence Name	5' Base Sequence 3'	
A-1	GAATTCTCTAGACTCCACCATGGTTAGAACCAGAGTCCTTTTCTGCCTCTTCATCTCTTTCTTCGCTACAGTCCAATCGAGCG	83mer
A-2	GTCCAATCGAGCGCTACACTCATCTCCACTTCATGCATTTCTCAGGCTGCACTGTACCAGTTCGGATGCTCAAGCAAGTCAAA	83mer
A-3	CAAGCAAGTCAAAGTCTTGCTACTGCAAGAACATCAATTGGCTCGGAAGCGTCACTGCATGCGCTTATGAGAACTCCAAATCT	83mer
A-4	TCCAGTGTGTAAACCTTGATACTTGAGCATTGGCTGGCAAGTTTCATCAAAGCGGAGTCCAGAGTCTTGTTAGATTTGGAGTT	83mer
A-5	TGTCTTCTTATCGGATTTCTCAGGAGCGCGAAGGTAGTTACTTGCATTAAGGTAGATGTTCTTCATGTCCTCCAGTGTGTAAA	83mer
A-6	GGATCCCATAGTTTTCCTCATAGTAGTAGTGATAGGCCGTCTCATTTGCCATCAACGGTTGTGAAACAACTGTCTTCTTATCG	83mer
B-1	GGATCCACTTGAATTTGATGCGATCTCAATGGTGCGCATGGGGCCTCGTCTTCTTCTGGGTCGCAGTCCTTACCGCCGCA	80mer
B-2	CCTTACCGCCGCAACTATCTTGAACATTCTCAAACGCGTATTCGGCAAGAACATTATGGCAAATTCTGTTAAGAAGTCTC	80mer
B-3	GTTAAGAAGTCTCTTATCTACCCAAGCGTTTACAAAGACTACAACGAGAGAACTTTCTATCTTTGGAAACGTTTGCCATT	80mer
B-4	AGAGTGAGAGAATAGTCAGAATGACAAAGATAAGAACTACGAGTCCTTTGCCTCGAGTTGTAAAGTTGAATGGCAAACGT	80mer
B-5	AATGCCATTGATCTTCTCCATCTAGGTCTATCGTAAGGATGTGGCAACTTGATGTTATGTCCGAAAGAGAGTGAGAGAAT	80mer
B-6	TCCGGATACCGAAAAGGTACACCACGGGGAAAAGAGCGATTGCCATCAAGTCAGCACGGCGTGAGACGAATGCCATTGAT	80mer
C-1	TCCGGAACAACCCCTTCATCCCAATCACCGGATTGAGCTTTAGTACTTTCAACTTTTACCACAAATGGTCAGCATACGTCTGC	83mer
C-2	GCATACGTCTGCTTCATGTTAGCCGTCGTCCATTCAATCGTTATGACCGCTTCAGGAGTTAAACGAGGAGTATTCCAGTCTCT	83mer
C-3	TATTCCAGTCTCTTGTAAGGAAATTCTACTTCAGATGGGGAATAGTAGCCACAATTCTTATGTCCATCATCATTTTCCAGTCC	83mer
C-4	ATAAACATGATGTTCATGGCTTTGTGAATAAGTAAGAAGATTTCATAACCTCGGTTCCTGAAGACCTTCTCGGACTGGAAAAT	83mer
C-5	GAGGATGCCAGCCATGGACCAGATCCAGCCCATCCATCCTAGTGTGTGGCAATGGTAATACATAGCTATGATAAACATGATGT	83mer
C-6	GTCGACAAAGTGGCGGTCTTAAGACCTCCGTTCATGATGATACGTACAATTCGGCAGAACCTGTCGAAGCAGAGGATGCCAGC	83mer

FIG. 6A

FIG. 6

FIG. 6A

FIG. 6B

D-1	GTCGACCACAGATGATTCTAACGTTATCAAGATCTCTGTCAAGAAGCCTAAGTTCTTCAAGTATCAAGTGGGAGCATTTGCC	82mer
D-2	GGAGCATTTGCCTATATGTACTTTCTTTCACCAAAATCAGCCTGGTTCTACAGTTTTCAATCTCATCCCTTCACAGTCCTAT	82mer
D-3	TTCACAGTCCTATCAGAAAGGCACAGAGATCCTAACAACCCAGATCAACTAACTATGTACGTCAAAGCTAACAAGGGCATTA	82mer
D-4	CCTCTAAGAAAATCTTGCAATCAACGGTATGGTTTGGAGCGCTTAGAACTTTGCTAAGAAGTACTCTCGTAATGCCCTTGTT	82mer
D-5	GGCCCGCAGCTACTCCTACTAGATTTGTCTTAAGTTTGGCAATGTGAGGGACAGTTACGCCATATGGTCCCTCTAAGAAAAT	82mer
D-6	CTGCAGTTGATCAGTGCTAGGCAATCTAAGGCATTCTACGAAATGGGGGTAGATGGCTGCCACGCCGAGGCCCGCAGCTACT	82mer

E-1	CTGCAGCACAAGTTCTACTGGATCGTCAACGACCTTAGTCACCTTAAGTGGTTCGAAAACGAGCTACAATGGCTTAA	77mer
E-2	ACAATGGCTTAAGGAGAAATCTTGTGAAGTCTCTGTCATCTACACTGGGTCATCAGTGGAGGATACAAACTCAGATG	77mer
E-3	CAAACTCAGATGAGTCCACTAAGGGTTTCGATGACAAGGAAGAATCTGAAATCACCGTAGAATGCCTTAACAAGAGG	77mer
E-4	GTGATGTTGTTGTTCTCGAGTTCTGACAATTTGATCTCTGATCTCACTAGCTCTTTGAGGTCTGGCCTCTTGTTAAG	77mer
E-5	CGATACCTTGTACAACTGCATTCCTAAAGTCGTCATTGAAAGTCGCTGGTCCGCATGAGTAGAAAGTGATGTTGTTG	77mer
E-6	AAGCTTGAGCTCTTACCAAGTAAAACTCTCCTCCTCTAGTTCGACATCTATCTTCAGACTAGAATCGATACCTTGTA	77mer

FIG. 6B

FIG. 7A

FIG. 7B

FIG. 7C

FIG. 7

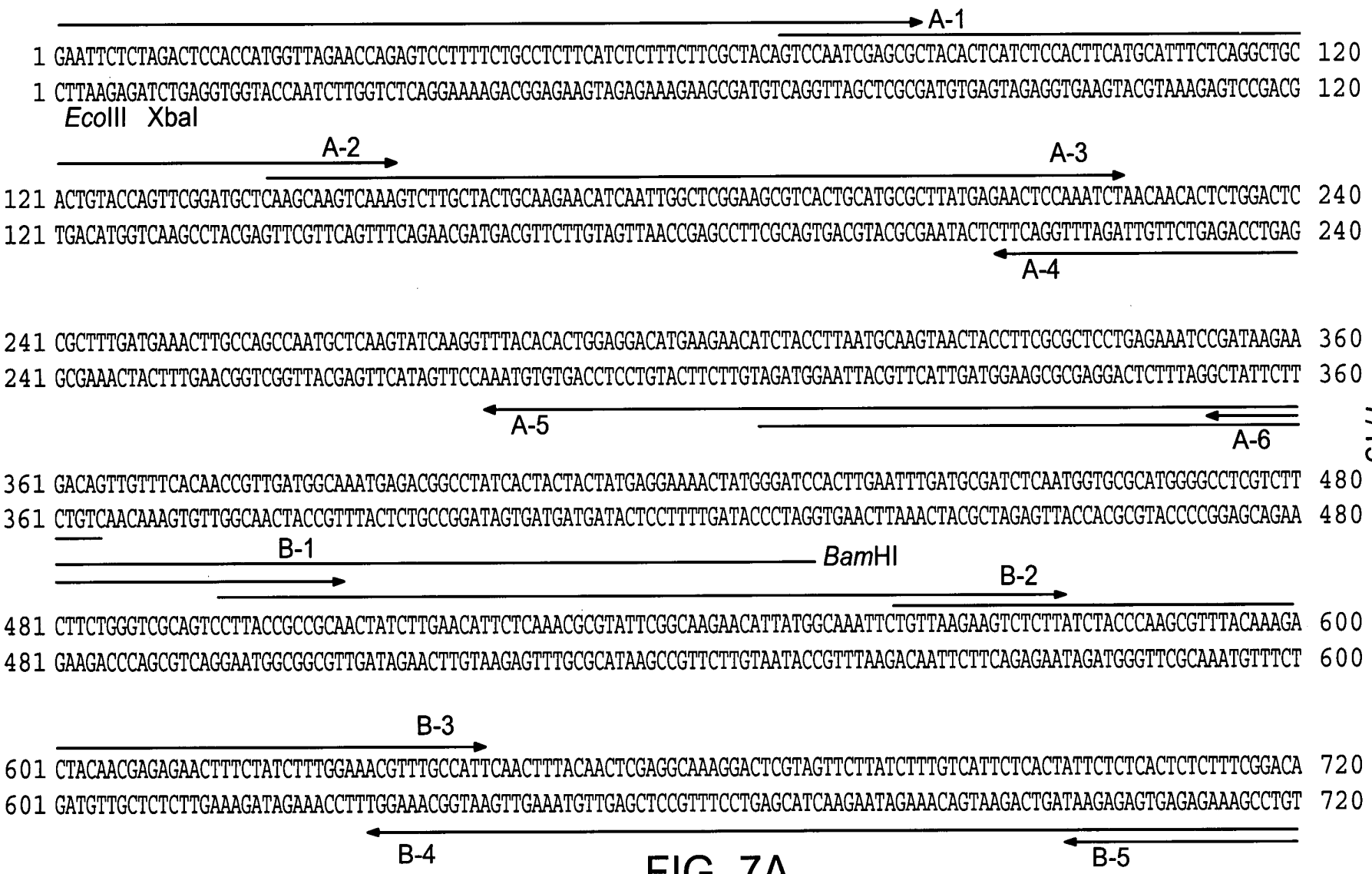

A-1
1 GAATTCTCTAGACTCCACCATGGTTAGAACCAGAGTCCTTTTCTGCCTCTTCATCTCTTTCTTCGCTACAGTCCAATCGAGCGCTACACTCATCTCCACTTCATGCATTTCTCAGGCTGC 120
1 CTTAAGAGATCTGAGGTGGTACCAATCTTGGTCTCAGGAAAAGACGGAGAAGTAGAGAAAGAAGCGATGTCAGGTTAGCTCGCGATGTGAGTAGAGGTGAAGTACGTAAAGAGTCCGACG 120
EcoIII XbaI
A-2
A-3
121 ACTGTACCAGTTCGGATGCTCAAGCAAGTCAAAGTCTTGCTACTGCAAGAACATCAATTGGCTCGGAAGCGTCACTGCATGCGCTTATGAGAACTCCAAATCTAACAACACTCTGGACTC 240
121 TGACATGGTCAAGCCTACGAGTTCGTTCAGTTTCAGAACGATGACGTTCTTGTAGTTAACCGAGCCTTCGCAGTGACGTACGCGAATACTCTTCAGGTTTAGATTGTTCTGAGACCTGAG 240
A-4
241 CGCTTTGATGAAACTTGCCAGCCAATGCTCAAGTATCAAGGTTTACACACTGGAGGACATGAAGAACATCTACCTTAATGCAAGTAACTACCTTCGCGCTCCTGAGAAATCCGATAAGAA 360
241 GCGAAACTACTTTGAACGGTCGGTTACGAGTTCATAGTTCCAAATGTGTGACCTCCTGTACTTCTTGTAGATGGAATTACGTTCATTGATGGAAGCGCGAGGACTCTTTAGGCTATTCTT 360
A-5
A-6
361 GACAGTTGTTTCACAACCGTTGATGGCAAATGAGACGGCCTATCACTACTACTATGAGGAAAACTATGGGATCCACTTGAATTTGATGCGATCTCAATGGTGCGCATGGGGCCTCGTCTT 480
361 CTGTCAACAAAGTGTTGGCAACTACCGTTTACTCTGCCGGATAGTGATGATGATACTCCTTTTGATACCCTAGGTGAACTTAAACTACGCTAGAGTTACCACGCGTACCCCGGAGCAGAA 480
B-1
BamHI
B-2
481 CTTCTGGGTCGCAGTCCTTACCGCCGCAACTATCTTGAACATTCTCAAACGCGTATTCGGCAAGAACATTATGGCAAATTCTGTTAAGAAGTCTCTTATCTACCCAAGCGTTTACAAAGA 600
481 GAAGACCCAGCGTCAGGAATGGCGGCGTTGATAGAACTTGTAAGAGTTTGCGCATAAGCCGTTCTTGTAATACCGTTTAAGACAATTCTTCAGAGAATAGATGGGTTCGCAAATGTTTCT 600
B-3
601 CTACAACGAGAGAACTTTCTATCTTTGGAAACGTTTGCCATTCAACTTTACAACTCGAGGCAAAGGACTCGTAGTTCTTATCTTTGTCATTCTCACTATTCTCTCACTCTCTTTCGGACA 720
601 GATGTTGCTCTCTTGAAAGATAGAAACCTTTGGAAACGGTAAGTTGAAATGTTGAGCTCCGTTTCCTGAGCATCAAGAATAGAAACAGTAAGACTGATAAGAGAGTGAGAGAAAGCCTGT 720
B-4
B-5

FIG. 7A

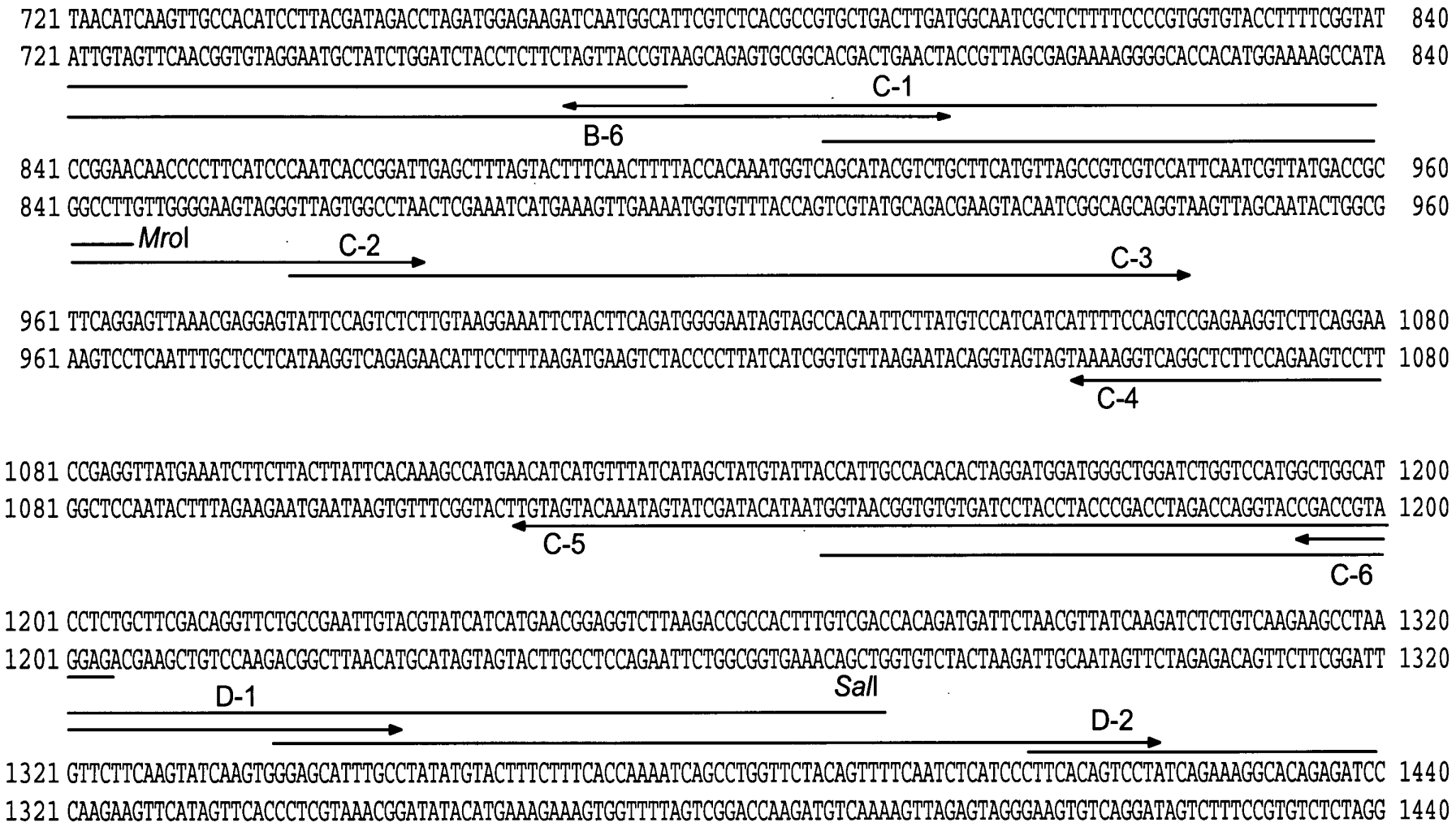

721 TAACATCAAGTTGCCACATCCTTACGATAGACCTAGATGGAGAAGATCAATGGCATTCGTCTCACGCCGTGCTGACTTGATGGCAATCGCTCTTTTCCCCGTGGTGTACCTTTTCGGTAT 840
721 ATTGTAGTTCAACGGTGTAGGAATGCTATCTGGATCTACCTCTTCTAGTTACCGTAAGCAGAGTGCGGCACGACTGAACTACCGTTAGCGAGAAAAGGGGCACCACATGGAAAAGCCATA 840
C-1
B-6
841 CCGGAACAACCCCTTCATCCCAATCACCGGATTGAGCTTTAGTACTTTCAACTTTTACCACAAATGGTCAGCATACGTCTGCTTCATGTTAGCCGTCGTCCATTCAATCGTTATGACCGC 960
841 GGCCTTGTTGGGGAAGTAGGGTTAGTGGCCTAACTCGAAATCATGAAAGTTGAAAATGGTGTTTACCAGTCGTATGCAGACGAAGTACAATCGGCAGCAGGTAAGTTAGCAATACTGGCG 960
MroI
C-2
C-3
961 TTCAGGAGTTAAACGAGGAGTATTCCAGTCTCTTGTAAGGAAATTCTACTTCAGATGGGGAATAGTAGCCACAATTCTTATGTCCATCATCATTTTCCAGTCCGAGAAGGTCTTCAGGAA 1080
961 AAGTCCTCAATTTGCTCCTCATAAGGTCAGAGAACATTCCTTTAAGATGAAGTCTACCCCTTATCATCGGTGTTAAGAATACAGGTAGTAGTAAAAGGTCAGGCTCTTCCAGAAGTCCTT 1080
C-4
1081 CCGAGGTTATGAAATCTTCTTACTTATTCACAAAGCCATGAACATCATGTTTATCATAGCTATGTATTACCATTGCCACACACTAGGATGGATGGGCTGGATCTGGTCCATGGCTGGCAT 1200
1081 GGCTCCAATACTTTAGAAGAATGAATAAGTGTTTCGGTACTTGTAGTACAAATAGTATCGATACATAATGGTAACGGTGTGTGATCCTACCTACCCGACCTAGACCAGGTACCGACCGTA 1200
C-5
C-6
1201 CCTCTGCTTCGACAGGTTCTGCCGAATTGTACGTATCATCATGAACGGAGGTCTTAAGACCGCCACTTTGTCGACCACAGATGATTCTAACGTTATCAAGATCTCTGTCAAGAAGCCTAA 1320
1201 GGAGACGAAGCTGTCCAAGACGGCTTAACATGCATAGTAGTACTTGCCTCCAGAATTCTGGCGGTGAAACAGCTGGTGTCTACTAAGATTGCAATAGTTCTAGAGACAGTTCTTCGGATT 1320
D-1
SalI
D-2
1321 GTTCTTCAAGTATCAAGTGGGAGCATTTGCCTATATGTACTTTCTTTCACCAAAATCAGCCTGGTTCTACAGTTTTCAATCTCATCCCTTCACAGTCCTATCAGAAAGGCACAGAGATCC 1440
1321 CAAGAAGTTCATAGTTCACCCTCGTAAACGGATATACATGAAAGAAAGTGGTTTTAGTCGGACCAAGATGTCAAAAGTTAGAGTAGGGAAGTGTCAGGATAGTCTTTCCGTGTCTCTAGG 1440

FIG. 7B

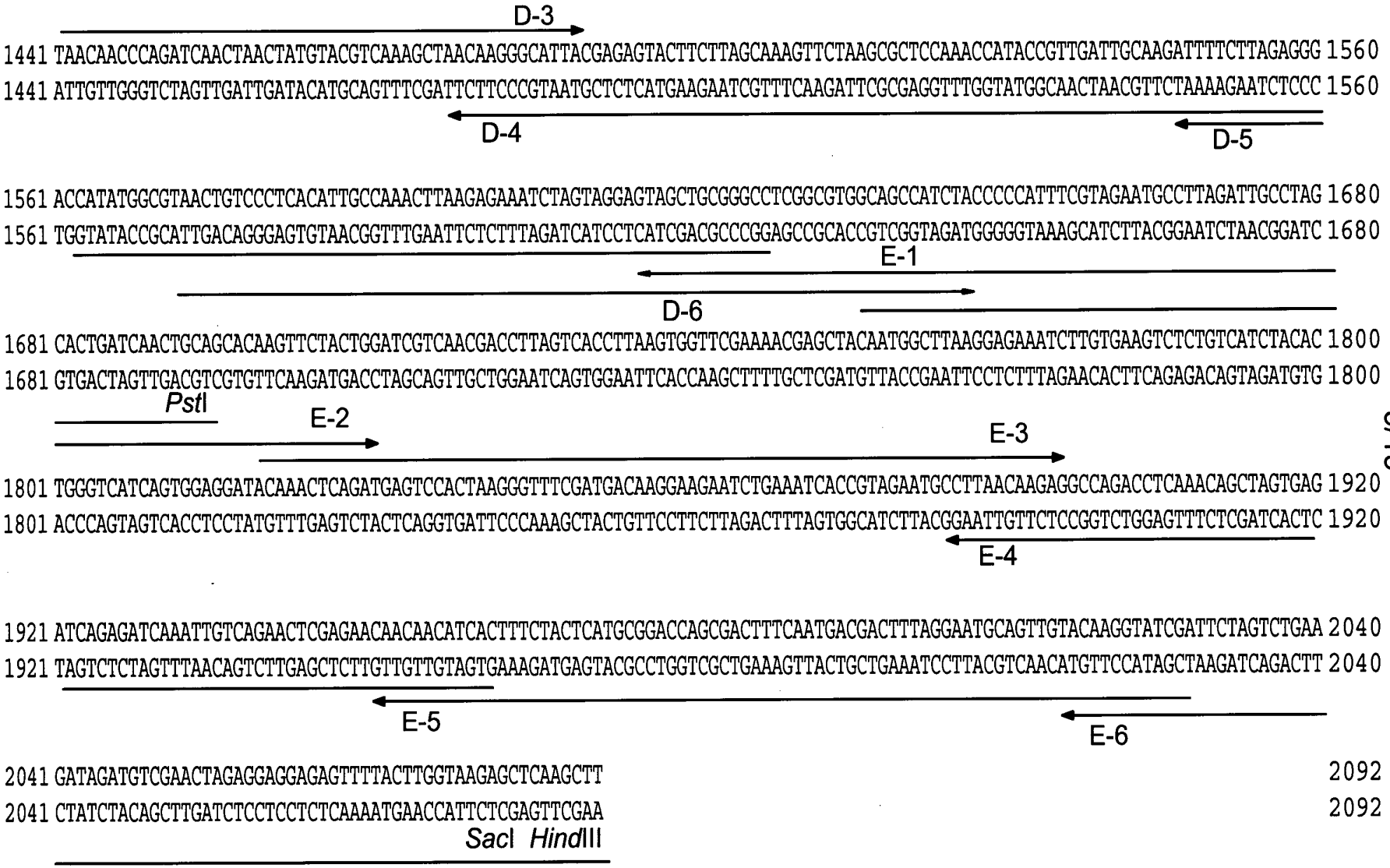

D-3
1441 TAACAACCCAGATCAACTAACTATGTACGTCAAAGCTAACAAGGGCATTACGAGAGTACTTCTTAGCAAAGTTCTAAGCGCTCCAAACCATACCGTTGATTGCAAGATTTTCTTAGAGGG 1560
1441 ATTGTTGGGTCTAGTTGATTGATACATGCAGTTTCGATTCTTCCCGTAATGCTCTCATGAAGAATCGTTTCAAGATTCGCGAGGTTTGGTATGGCAACTAACGTTCTAAAAGAATCTCCC 1560
D-4
D-5
1561 ACCATATGGCGTAACTGTCCCTCACATTGCCAAACTTAAGAGAAATCTAGTAGGAGTAGCTGCGGGCCTCGGCGTGGCAGCCATCTACCCCCATTTCGTAGAATGCCTTAGATTGCCTAG 1680
1561 TGGTATACCGCATTGACAGGGAGTGTAACGGTTTGAATTCTCTTTAGATCATCCTCATCGACGCCCGGAGCCGCACCGTCGGTAGATGGGGGTAAAGCATCTTACGGAATCTAACGGATC 1680
E-1
D-6
1681 CACTGATCAACTGCAGCACAAGTTCTACTGGATCGTCAACGACCTTAGTCACCTTAAGTGGTTCGAAAACGAGCTACAATGGCTTAAGGAGAAATCTTGTGAAGTCTCTGTCATCTACAC 1800
1681 GTGACTAGTTGACGTCGTGTTCAAGATGACCTAGCAGTTGCTGGAATCAGTGGAATTCACCAAGCTTTTGCTCGATGTTACCGAATTCCTCTTTAGAACACTTCAGAGACAGTAGATGTG 1800
PstI
E-2
E-3
1801 TGGGTCATCAGTGGAGGATACAAACTCAGATGAGTCCACTAAGGGTTTCGATGACAAGGAAGAATCTGAAATCACCGTAGAATGCCTTAACAAGAGGCCAGACCTCAAACAGCTAGTGAG 1920
1801 ACCCAGTAGTCACCTCCTATGTTTGAGTCTACTCAGGTGATTCCCAAAGCTACTGTTCCTTCTTAGACTTTAGTGGCATCTTACGGAATTGTTCTCCGGTCTGGAGTTTCTCGATCACTC 1920
E-4
1921 ATCAGAGATCAAATTGTCAGAACTCGAGAACAACAACATCACTTTCTACTCATGCGGACCAGCGACTTTCAATGACGACTTTAGGAATGCAGTTGTACAAGGTATCGATTCTAGTCTGAA 2040
1921 TAGTCTCTAGTTTAACAGTCTTGAGCTCTTGTTGTTGTAGTGAAAGATGAGTACGCCTGGTCGCTGAAAGTTACTGCTGAAATCCTTACGTCAACATGTTCCATAGCTAAGATCAGACTT 2040
E-5
E-6
2041 GATAGATGTCGAACTAGAGGAGGAGAGTTTTACTTGGTAAGAGCTCAAGCTT 2092
2041 CTATCTACAGCTTGATCTCCTCCTCTCAAAATGAACCATTCTCGAGTTCGAA 2092
SacI HindIII

FIG. 7C

FIG. 9A
FIG. 9B
FIG. 9C

FIG. 9

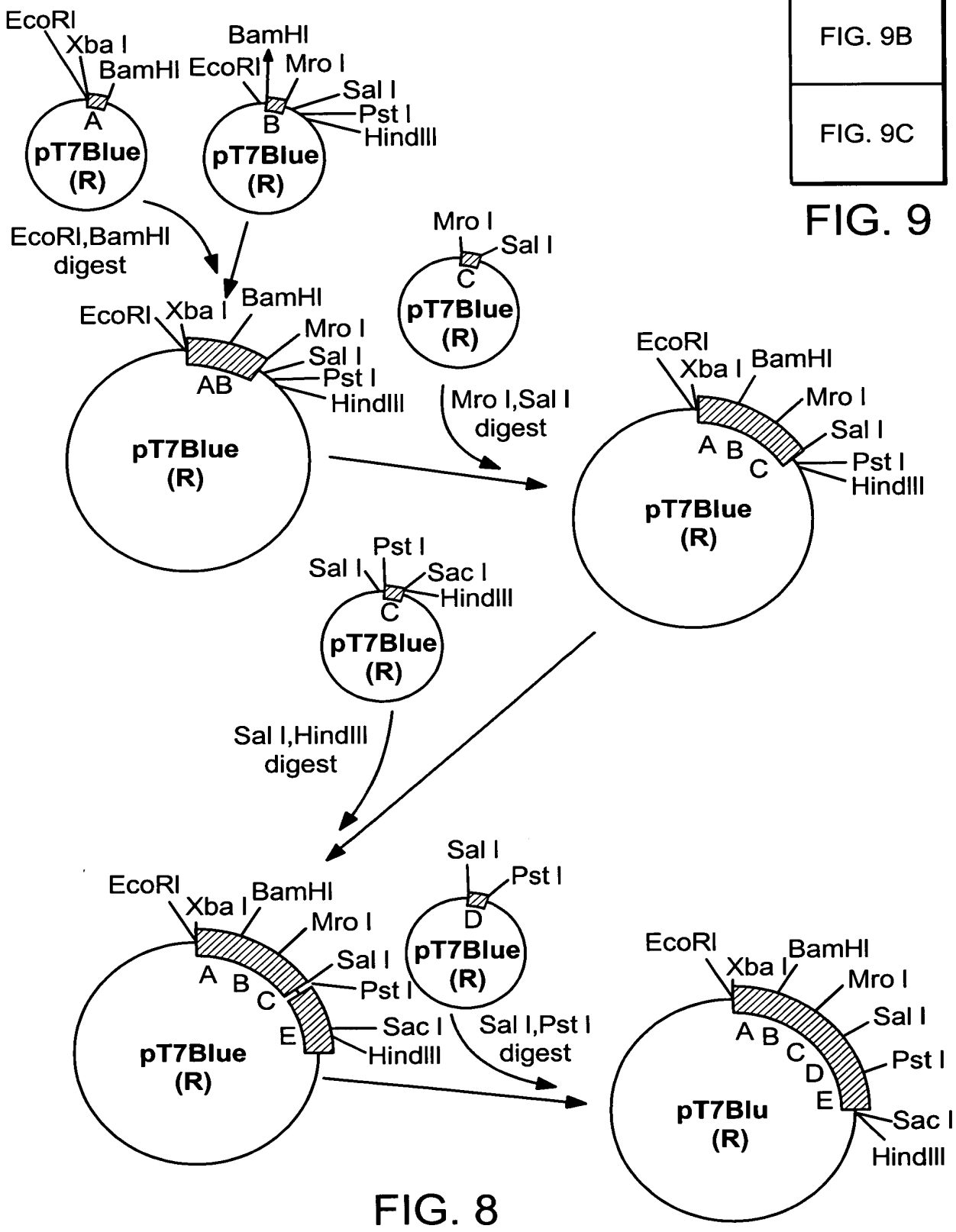


FIG. 8

```
   1                                                                gaattctctagactccacc  19

  20 ATGGTTAGAACCAGAGTCCTTTTCTGCCTCTTCATCTCTTTCTTCGCTACAGTCCAATCGAGCGCTACACTCATCTCCACTTCATGCATT 109
   1  M  V  R  T  R  V  L  F  C  L  F  I  S  F  F  A  T  V  Q  S  S  A  T  L  I  S  T  S  C  I  30

 110 TCTCAGGCTGCACTGTACCAGTTCGGATGCTCAAGCAAGTCAAAGTCTTGCTACTGCAAGAACATCAATTGGCTCGGAAGCGTCACTGCA 109
  31  S  Q  A  A  L  Y  Q  F  G  C  S  S  K  S  K  S  C  Y  C  K  N  I  N  W  L  G  S  V  T  A  60

 200 TGCGCTTATGAGAACTCCAAATCTAACAAGACTCTGGACTCCGGTTTGATGAAACTTGCCAGCCAATGCTCAAGTATCAAGGTTTACACA 289
  61  C  A  Y  E  N  S  K  S  N  K  T  L  D  S  A  L  M  K  L  A  S  Q  C  S  S  I  K  Y  Y  T  90

 290 CTGGAGGACATGAAGAACATCTACCTTAATGCAAGTAACTACCTTCGCGCTCCTGAGAAATCCGATAAGAAGACAGTTGTTTCACAACCG 379
  91  L  E  D  M  K  N  I  Y  L  N  A  S  N  Y  L  R  A  P  E  K  S  D  K  K  T  V  V  S  Q  P 120

 380 TTGATGGCAAATGAGACGGCCTATCACTACTACTATGAGGAAAACTATGGGATCCACTTGAATTTGATGCGATCTCAATGGTGCGCATGG 469
 121  L  M  A  N  E  T  A  Y  H  Y  Y  Y  E  E  N  Y  G  I  H  L  N  L  M  R  S  Q  M  C  A  W 150

 470 GGCCTCGTCTTCTTCTGGGTCGCAGTCCTTACCGCCGCAACTATCTTGAACATTCTCAAACGCGTATTCGGCAAGAACATTATGGCAAAT 559
 151  G  L  V  F  F  W  V  A  V  L  T  A  A  T  I  L  N  I  L  K  R  V  F  G  K  N  I  M  A  N 180

 560 TCTGTTAAGAAGTCTCTTATCTACCCAAGCGTTTACAAAGACTACAACGAGAGAACTTTCTATCTTTGGAAACGTTTGCCATTCAACTTT 649
 181  S  V  K  K  S  L  I  Y  P  S  V  Y  K  O  Y  N  E  R  T  F  Y  L  N  K  R  L  P  F  N  F 210
```

FIG. 9A

```
650 ACAACTCGAGGCAAAGGACTCGTAGTTCTTATCTTTGTCATTCTGACTATTCTCTCACTCTCTTTCGGACATAACATCAAGTTGCCACAT 739
211  T  T  R  G  K  G  L  V  V  L  I  F  V  I  L  T  I  L  S  L  S  F  G  H  N  I  K  L  P  H  210

740 CCTTACGATAGACCTAGATGGAGAAGATCAATGGCATTCGTCTCACGCCGTGCTGACTTGATGGCAATCGCTCTTTTCCCCGTGGTGTAC 829
241  P  Y  D  R  P  R  W  R  R  S  M  A  F  V  S  R  R  A  D  L  M  A  I  A  L  F  P  V  V  Y  270

830 CTTTTCGGTATCCGGAACAACCCCTTCATCCCAATCACCGGATTGAGCTTTAGTACTTTCAACTTTTACCACAAATGGTCAGCATACGTC 919
271  L  F  G  I  R  N  N  P  F  I  P  I  T  G  L  S  F  S  T  F  N  F  Y  H  K  W  S  A  Y  V  300

920 TGCTTCATGTTAGCCGTCGTCCATTCAATCGTTATGACCGCTTCAGGAGTTAAACGAGGAGTATTCCAGTCTCTTGTAAGGAAATTCTAC 1009
301  C  F  M  L  A  V  V  H  S  I  V  M  T  A  S  G  V  K  R  G  V  F  G  S  L  V  R  K  F  Y  330

1010 TTCAGATGGGGAATAGTAGCCACAATTCTTATGTCCATCATCATTTTCCAGTCCGAGAAGGTCTTCAGGAACCGAGGTTATGAAATCTTC 1099
331  F  R  W  G  I  V  A  T  I  L  M  S  I  I  I  F  Q  S  E  K  V  F  R  N  R  G  Y  E  I  F  360

1100 TTACTTATTCACAAAGCCATGAACATCATGTTTATCATAGCTATGTATTACCATTGCCACACACTAGGATGGATGGGCTGGATCTGGTCC 1189
361  L  L  I  H  K  A  M  N  I  M  F  I  I  A  M  Y  Y  H  C  H  T  L  G  W  M  G  W  I  W  S  390

1190 ATGGCTGGCATCCTCTGCTTCGACAGGTTCTGCCGAATTGTACGTATCATCATGAACGGAGGTCTTAAGACCGCCACTTTGTCGACCACA 1279
391  M  A  G  I  L  C  F  D  R  F  C  R  I  V  R  I  I  M  N  G  G  L  K  T  A  T  L  S  T  T  420

1280 GATGATTCTAACGTTATCAAGATCTCTGTCAAGAAGCCTAAGTTCTTCAAGTATCAAGTGGGAGCATTTGCCTATATGTACTTTCTTTCA 1369
421  D  D  S  N  V  I  K  I  S  V  K  K  P  K  F  F  K  Y  Q  V  G  A  F  A  Y  M  Y  F  L  S  450

1370 CCAAAATCAGCCTGGTTCTACAGTTTTCAATCTCATCCCTTCACAGTCCTATCAGAAAGGCACAGAGATCCTAACAACCCAGATCAACTA 1459
451  P  K  S  A  W  F  Y  S  F  Q  S  H  P  F  T  V  L  S  E  R  N  R  D  P  N  N  P  D  Q  L  480
```

FIG. 9B

```
1460 ACTATGTACGTCAAAGCTAACAAGGGCATTACGAGAGTACTTCTTAGCAAAGTTCTAAGCGCTCCAAACCATACCGTTGATTGCAAGATT 1549
 481  T  M  Y  Y  K  A  N  K  G  I  T  R  V  L  L  S  K  Y  L  S  A  P  N  H  T  V  D  C  K  I  510
1550 TTCTTAGAGGGACCATATGGCGTAACTGTCCCTCACATTGCCAAACTTAAGAGAAATCTAGTAGGAGTAGCTGCGGGCCTCGGCGTGGCA 1639
 571  F  L  E  G  P  Y  G  V  T  V  P  H  I  A  K  L  K  R  N  L  V  G  V  A  A  G  L  G  V  A  570
1640 GCCATCTACCCCCATTTCGTAGAATGCCTTAGATTGCCTAGCACTGATCAACTGCAGCACAAGTTCTACTGGATCGTCAACGACCTTAGT 1729
 541  A  I  Y  P  H  F  V  E  C  L  R  L  P  S  T  D  Q  L  Q  H  K  F  Y  W  I  V  N  D  L  S  570
1730 CACCTTAAGTGGTTCGAAAACGAGCTACAATGGCTTAAGGAGAAATCTTGTGAAGTCTCTGTCATCTACACTGGGTCATCAGTGGAGGAT 1819
 571  H  L  K  W  F  E  N  E  L  Q  W  L  K  E  K  S  C  E  V  S  V  I  Y  T  G  S  S  V  E  D  600
1820 ACAAACTCAGATGAGTCCACTAAGGGTTTCGATGACAAGGAAGAATCTGAAATCACCGTAGAATGCCTTAACAAGAGGCCAGACCTCAAA 1909
 601  T  N  S  D  E  S  T  K  G  F  D  D  K  E  E  S  E  I  T  V  E  C  L  N  K  R  P  D  L  K  630
1910 GAGCTAGTGAGATCAGAGATCAAATTGTCAGAACTCGAGAACAACAACATCACTTTCTACTCATGCGGACCAGCGACTTTCAATGACGAC 1999
 631  E  L  V  R  S  E  I  K  L  S  E  L  E  N  N  N  I  T  F  Y  S  C  G  P  A  T  F  N  D  D  660
2000 TTTAGGAATGCAGTTGTACAAGGTATCGATTCTAGTCTGAAGATAGATGTCGAACTAGAGGAGGAGAGTTTTACTTGGTAA       2089
 661  F  R  N  A  V  V  Q  G  I  D  S  S  L  K  I  D  V  E  L  E  E  E  S  F  T  W  *        687
2090 ctt
```

FIG. 9C

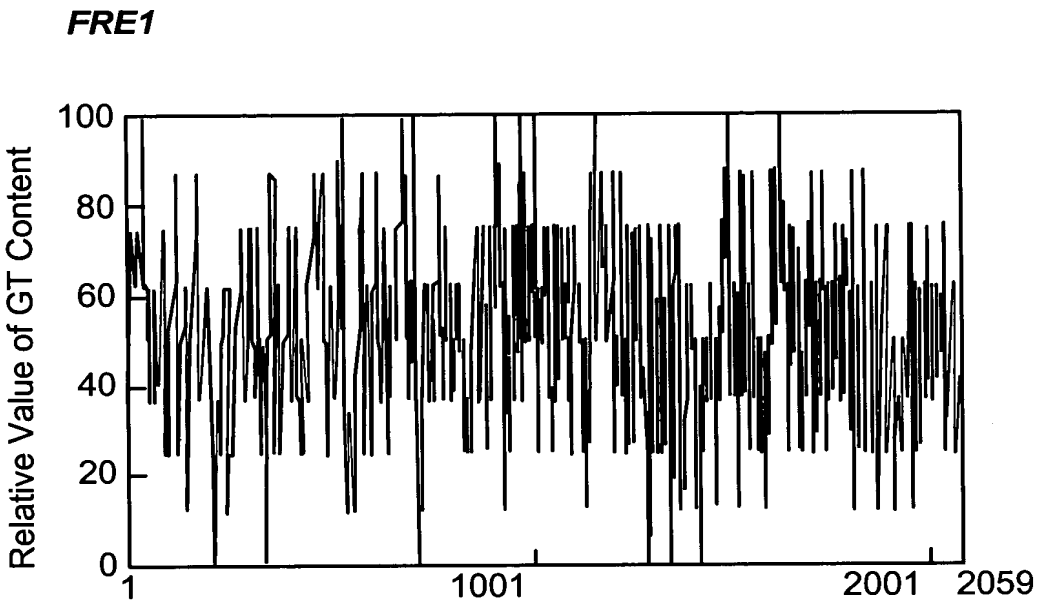


FIG. 10A

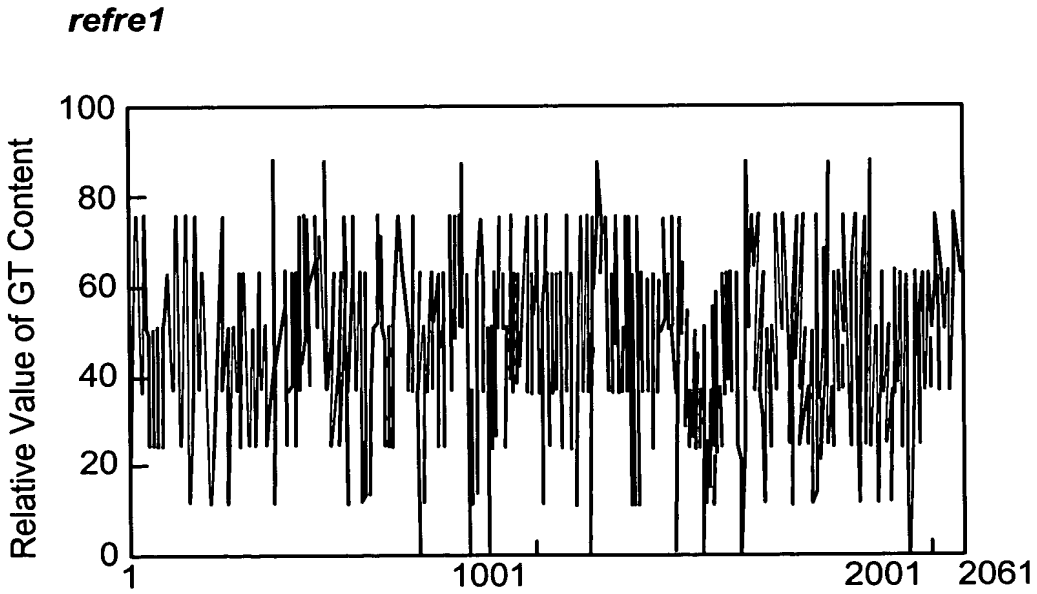


FIG. 10B

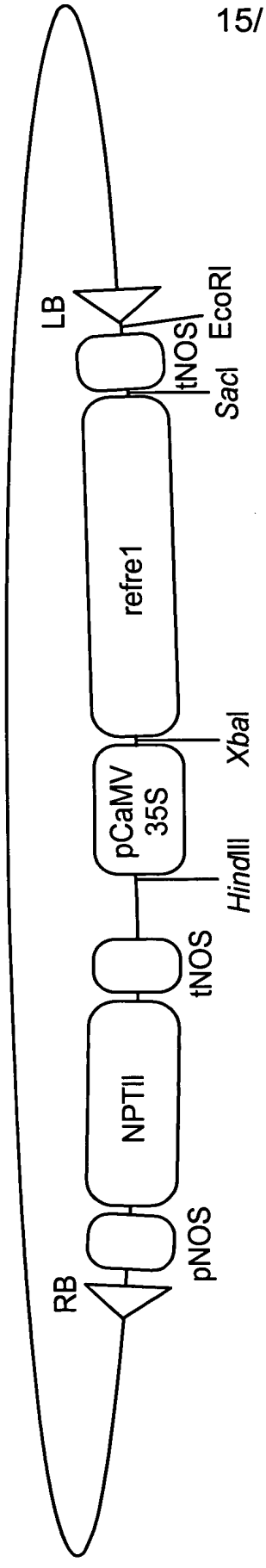

LB
tNOS
EcoRI
SacI
refre1
pCaMV 35S
XbaI
HindIII
tNOS
NPTII
pNOS
RB

FIG. 11

FIG. 13

FIG. 12

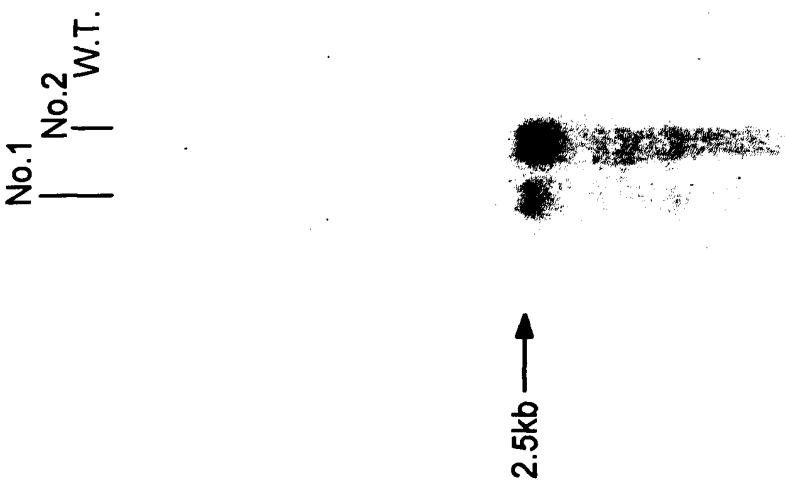

No.1
No.2
W.T.
2.5kb

FIG. 15

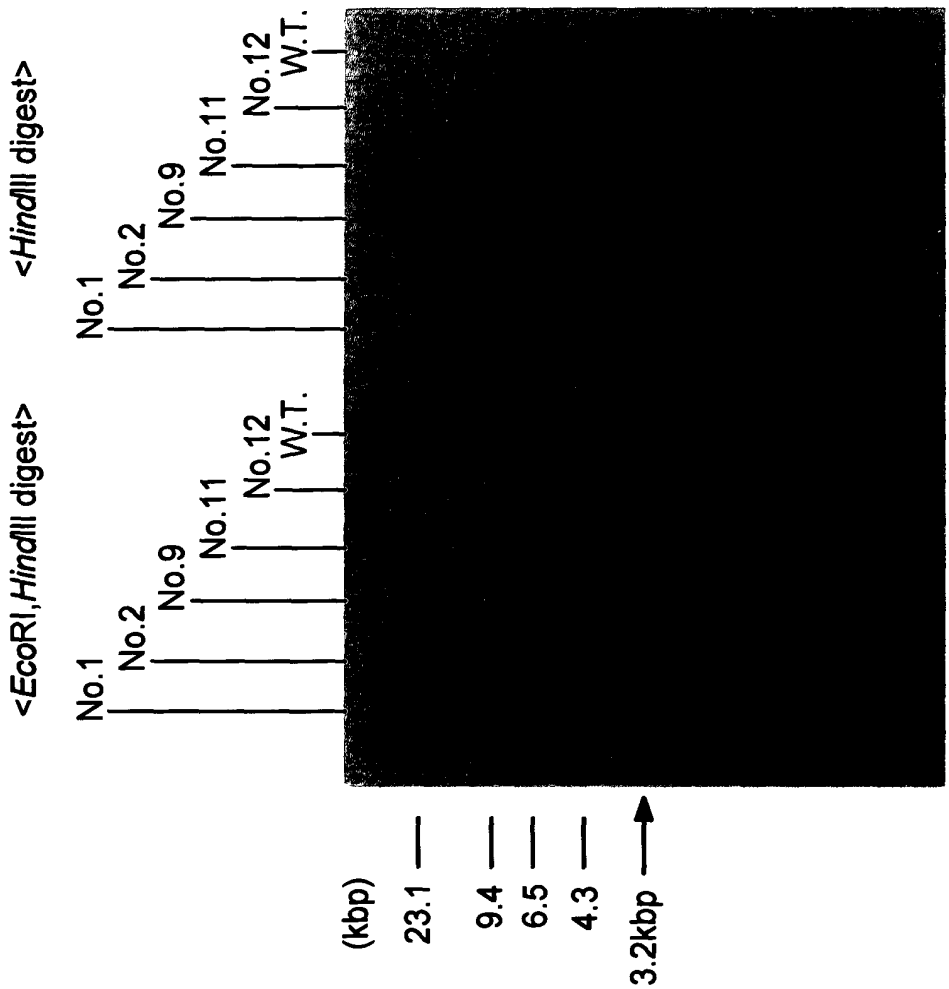

<EcoRI,HindIII digest>
No.1
No.2
No.9
No.11
No.12
W.T.
<HindIII digest>
No.1
No.2
No.9
No.11
No.12
W.T.
(kbp)
23.1
9.4
6.5
4.3
3.2kbp

FIG. 14

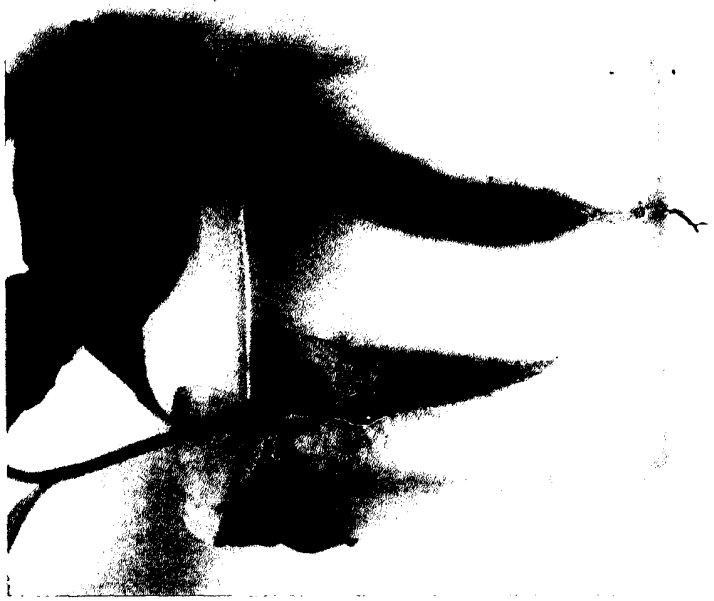


FIG. 17

FIG. 16

T_2 Plants

FIG. 18